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Abstract title	Among genes heterogeneity of the phylogenetic signal in genome data
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Abstract text	

Genome-scale inference of phylogeny has reduced the stochasticity associated with single gene phylogenies, but some drawbacks of this approach are not yet understood, particularly the among-gene heterogeneity of the phylogenetic signal. I studied this issue in *Drosophila* using two genome-scaled datasets. Although both datasets *apparently* resolve most of the relationships with high support when analysed at the nucleotide level, there are at least two types of incongruences. First, the phylogenetic signal is not homogenously distributed among nuclear, mitochondrial, and non-coding genes. Second, the phylogenetic signal is not homogenously distributed among ontology classes, whereby nuclear genes involved with the metabolism tend to carry their own signal. Most, but not all of these incongruences, are due to substitutions at synonymous sites which I show being affected by different mutational pressures in different types of data. Counter intuitively, partitioning is not successful in disclosing these incongruences, which are instead revealed by using across-site heterogeneous models or coalescent aware approaches. These results advocate that care should be taken when interpreting high supports from the analysis of genome data at the genus level. Phylogenetic incongruences may be however extremely instructive in revealing peculiar aspects of species biology such as introgression or incomplete lineage sorting.

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